

Applicant: Jay Short, et al.  
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Page 5

--42. (New) The method of claim 19, wherein each clone contains DNA obtained from a single organism.--

*B/Cmt*  
--43. (New) The method of claim 19, wherein the library is a multispecies library.--

--44. (New) The method of claim 43, wherein the library is generated from a mixed population of uncultured organisms.--

--45. (New) The method of claim 43, wherein the library is generated from isolates.--

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*add E3*  
**In The Specification**

Applicants respectfully request entry of the following amendments:

*On page 69, line 11, following the identified forward primer, please insert --(SEQ ID NO:1)--.*  
*On page 69, line 13, following the identified reverse primer, please insert --(SEQ ID NO:2)--.*

**REMARKS**

The present remarks are in response to the Office Action mailed December 7, 1999.

Claims 1-18 have been canceled without prejudice. New claims 19-45 have been added. Claims 1-18 were pending before this response. Original claim 18 was indicated to be "allowable if rewritten to overcome the rejection(s) under 35 USC 112, 2<sup>nd</sup> paragraph and to include all of the limitations of the base claim and any intervening claims (Office Action, page 13). By the present communication, claims 1-18 having been canceled and replaced with claims 19-45. These amendments add no new matter as the language of the new claims is fully supported by the specification and original claims.

The present invention provides methods for identifying a bioactivity or biomolecule of interest using high throughput screening of DNA by screening a library containing a plurality of clones obtained from more than one organism. Preferably, each clone contains DNA obtained